

SEQUENCE LISTING

(1) GENERAL INFORMATION:

15 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0. Version #1.30

(ii) TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL INTERACTION

25 (iii) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO:1:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (iii) MOLECULE TYPE - RNA

(iii) UNPUBLISHED - NO

10 (iv) ANTI SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

45 ATGAGTGACT CCAAGGAACC AAGACTGCAG CAGCTGGGCC TCCTGGAGGA GGAACAGCTG 60
AGAGGCCCTT GATTCCGACA GACTCGAGGA TACAAGAGCT TAGCAGGGTG TCTTGGCCAT 120
GGTCCCCCTGG TGCTGCAACT CCTCTCCTTC ACGCTTTGG CTGGGCTCCT TGTCCAAGTG 180
50 TCCAAGGTCC CCAGCTCCAT AAGTCAGGAA CAATCCAGGC AAGACGCGAT CTACCAGAAC 240
CTGACCCAGC TTAAAGCTGC AGTGGGTGAG CTCTCAGAGA AATCCAAGCT GCAGGAGATC 300
55 TACCAGGAGC TGACCCAGCT GAAGGCTGCA GTGGGTGAGC TTCCAGAGAA ATCTAAGCTG 360

CAGGAGATCT ACCAGGAGCT GACCCGGCTG AAGGCTGCAG TGGGTGAGCT TCCAGAGAAA 420
 5 TCTAAGCTGC AGGAGATCTA CCAGGAGCTG ACCTGGCTGA AGGCTGCAGT GGGTGAGCTT 480
 CCAGAGAAAT CTAAGATGCA GGAGATCTAC CAGGAGCTGA CTCGGCTGAA GGCTGCAGTG 540
 GGTGAGCTTC CAGAGAAATC TAAGCAGCAG GAGATCTACC AGGAGCTGAC CCGGCTGAAG 600
 10 GCTGCAGTGG GTGAGCTTCC AGAGAAATCT AAGCAGCAGG AGATCTACCA GGAGCTGACC 660
 CGGCTGAAGG CTGCAGTGGG TGAGCTTCCA GAGAAATCTA AGCAGCAGGA GATCTACCAG 720
 15 GAGCTGACCC AGCTGAAGGC TGCACTGGAA CGCCTGTGCC ACCCCTGTCC CTGGGAATGG 780
 ACATTCTTCC AAGGAAACTG TTACTTCATG TCTAACTCCC AGCGGAAC TG GCACGACTCC 840
 ATCACCGCCT GCAAAGAAGT GGGGGCCAG CTCGTGTAA TCAAAAGTGC TGAGGAGCAG 900
 20 AACTTCCTAC AGCTGCAGTC TTCCAGAAAGT AACCGCTTCA CCTGGATGGG ACTTTCAGAT 960
 CTAATCAGG AAGGCACGTG GCAATGGGTG GACGGCTCAC CTCTGTTGCC CAGCTTCAAG 1020
 CAGTATTGGA ACAGAGGAGA GCCCAACAAC GTTGGGGAGG AAGACTGCGC GGAATTTAGT 1080
 25 GGCAATGGCT GGAACGACGA CAAATGTAAT CTTGCCAAAT TCTGGATCTG CAAAAAGTCC 1140
 GCAGCCTCCT GCTCCAGGGA TGAAGAACAG TTTCTTCTC CAGCCCCTGC CACCCCAAAC 1200
 30 CCCCTCCTG CGTAG 1215

2) INFORMATION FOR SEQ ID NO:2:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45 Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu
 1 5 10 15

Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly
 20 25 30

50 Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu
 35 40 45

55 Gln Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val
 50 55 60

Ser Lys Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp
 65 70 75
 Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu
 5 80 85 90
 Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
 95 100 105
 10 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu
 110 115 120
 Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly
 125 130 135
 15 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu
 140 145 150
 Thr Trp Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys
 20 155 160 165
 Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val
 170 175 180
 25 Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu
 185 190 195
 Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser
 30 200 205 210
 Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala
 215 220 225
 35 Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
 230 235 240
 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro
 245 250 255
 40 Cys Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met
 260 265 270
 Ser Asn Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys
 45 275 280 285
 Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln
 290 295 300
 50 Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp
 305 310 315
 Met Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val
 55 320 325 330

Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg
335 340 345

5 Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser
350 355 360

Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp
365 370 375

10 Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln
380 385 390

Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala *

395 400 404